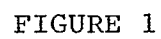


## 1 / 8



2/8

## REPLACEMENT SHEET

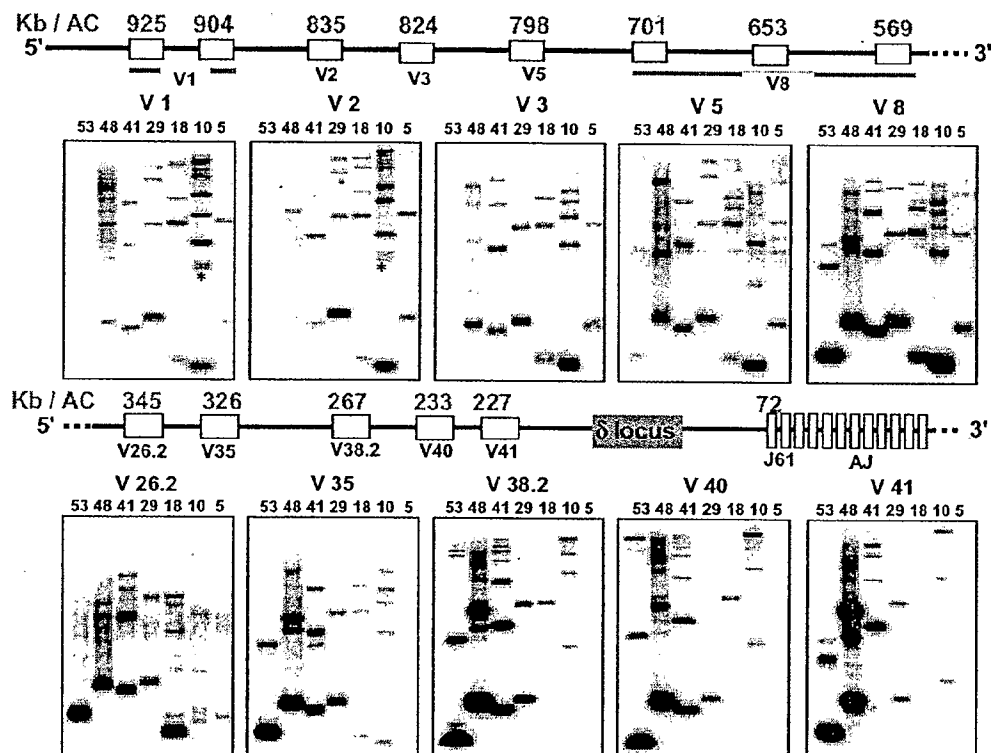


FIGURE 2

3/8

## REPLACEMENT SHEET

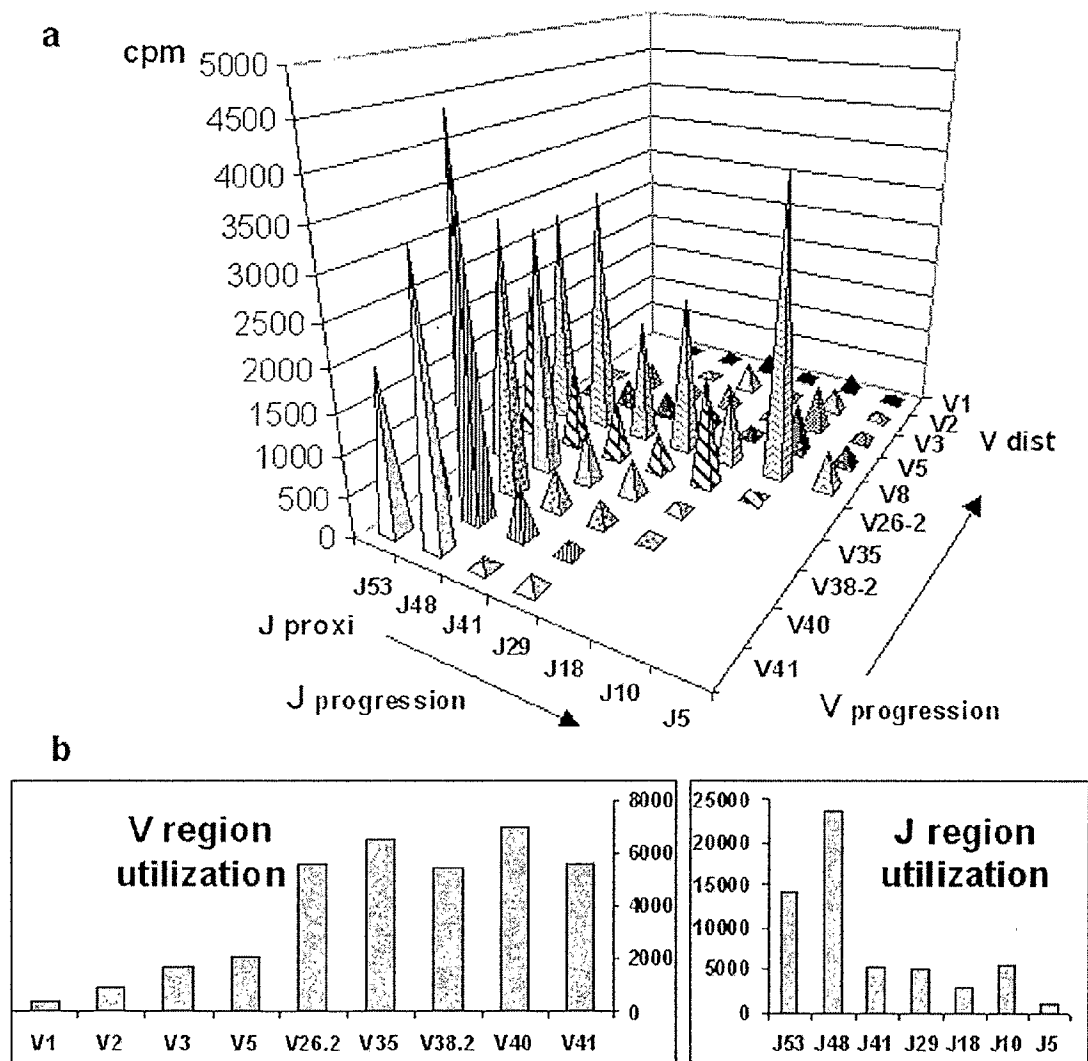


FIGURE 3

REPLACEMENT SHEET

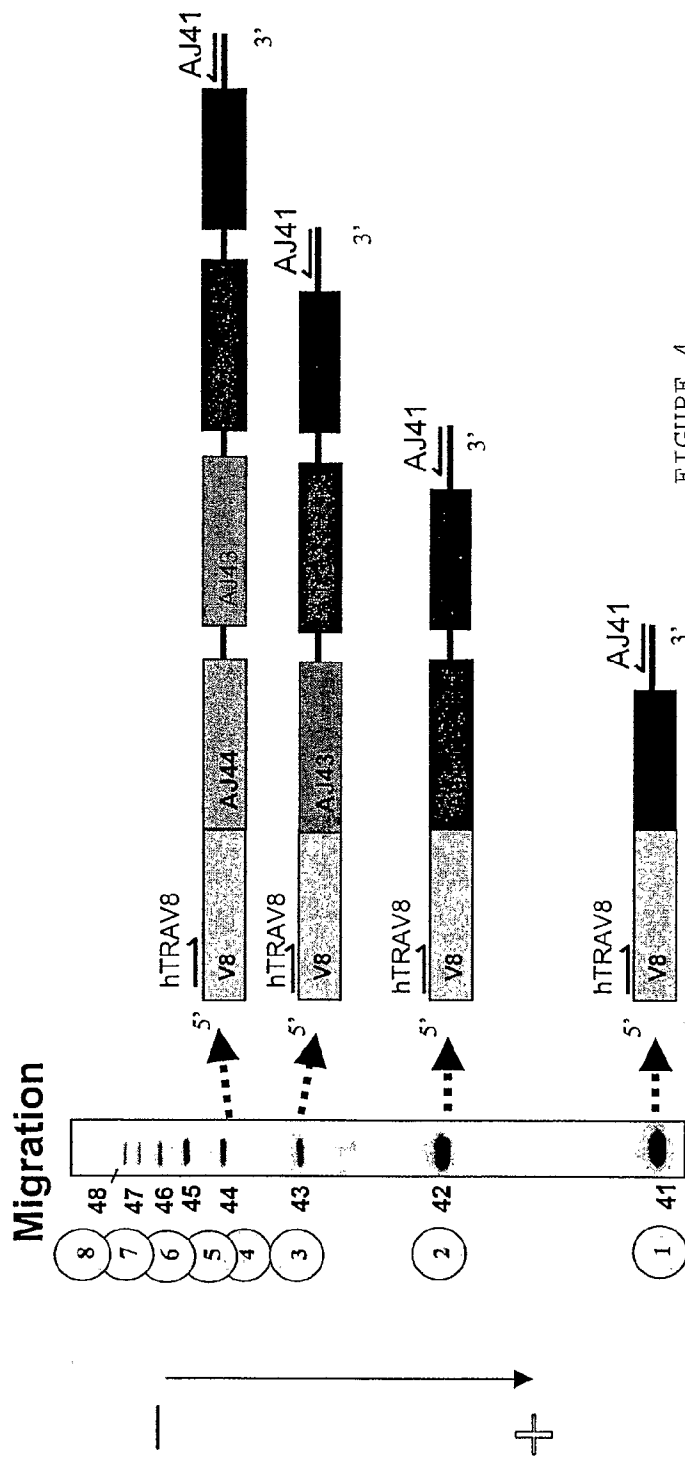
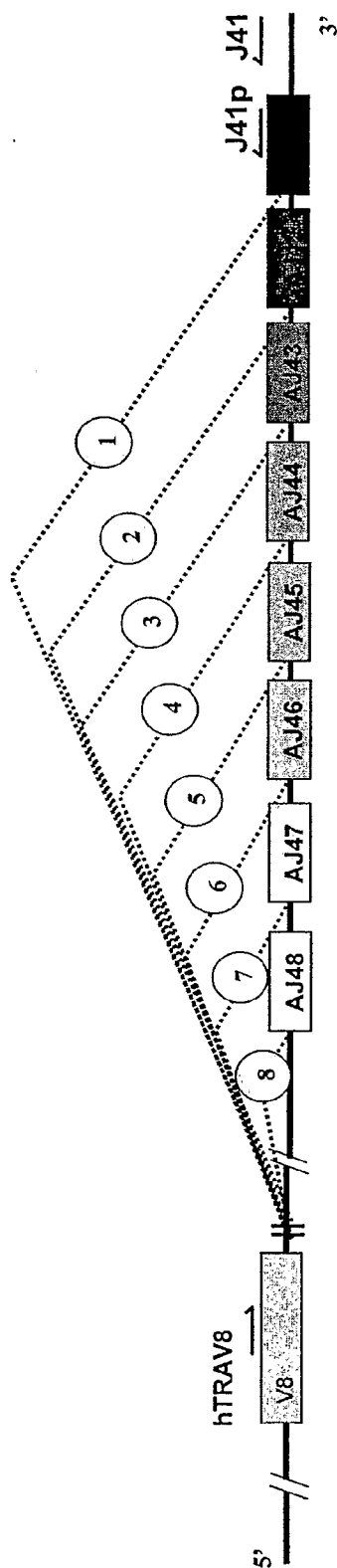


FIGURE 4

# REPLACEMENT SHEET

hv gene	Heptamer	SEQ ID NO	%	Spacer	SEQ ID NO	%	Nonamer	SEQ ID NO	%	RSS score	Dist/Ca (Kb)	Signal Qty	J tropism
hV1-1	CACAGTG	76	100	ACTATGAGGCCCTCCCTTAACGTGTG	77	56	CCAAAAATTC	78	56	72	925	1604	J10
hV1-2	CACGGTG	79	86	ACTATGAGGCCCTCTTAGCTGCA	80	63	CCAAAAATTC	78	56	69	904		J10
hV2	CACAGAG	81	86	GCAGGGAACCCATGAAGAGCTGA	82	56	ACAGAAACA	83	78	75	835	1637	J10
hV3	CACACTG	84	86	ATAGGGCTGCAGGGGAGCAGA	85	56	ACACAAACT	86	89	80	824	1940	J10
hV5	CACATTG	87	86	CTTCTCAGGCACTCTGATCCCTGT	88	94	ACCCAAACC	89	100	93	798	2406	J10
hV8-2	CACAGTG	76	100	CTTGAGACTGCAGGAGAGCTGAA	90	50	CACAAGCCT	91	33	63	701		All J area
hV8-4	CACAGTG	76	100	CTTGAGACTGCAGGAGAGCTGAA	90	50	CATAAACCT	92	33	63	653	15830	
hV8-6	CACAGTG	76	100	CCTGAGACTGCAGGAGAGCTGAA	93	44	CACAAGCCT	94	44	65	569		
hV26-2	CACAGTG	76	100	GGACAGATGGGGCTGAGCTGTG	95	56	CAATATCTC	96	33	64	345	5638	J48
hV35	CACAGTG	76	100	CTCCCCAAACACCTGAGCCTGT	97	94	ACTCAAAC	98	78	90	326	6520	J48
hV38-2	CACAGTG	76	100	AGACAAGCAACAGGAGAGGCTT	99	31	ACAGAAACC	100	89	78	267	11008	J48
hV40	CACATGTG	101	86	TAAAAAGCACAGTGGGAGCTATA	102	44	CAAAAACT	103	44	60	233	6930	J48
hV41	CACAGTG	76	100	CTCCCAGGCACTGGAGCCCGT	104	94	ACCTTAACT	105	78	90	227	5630	J48
<b>Consensus</b>	CACAGTG	76		-T---CAG-CA-CTG-AACCTGT G GC GC GG	106		ACACAAACC C	107		%			

FIGURE 5

REPLACEMENT SHEET

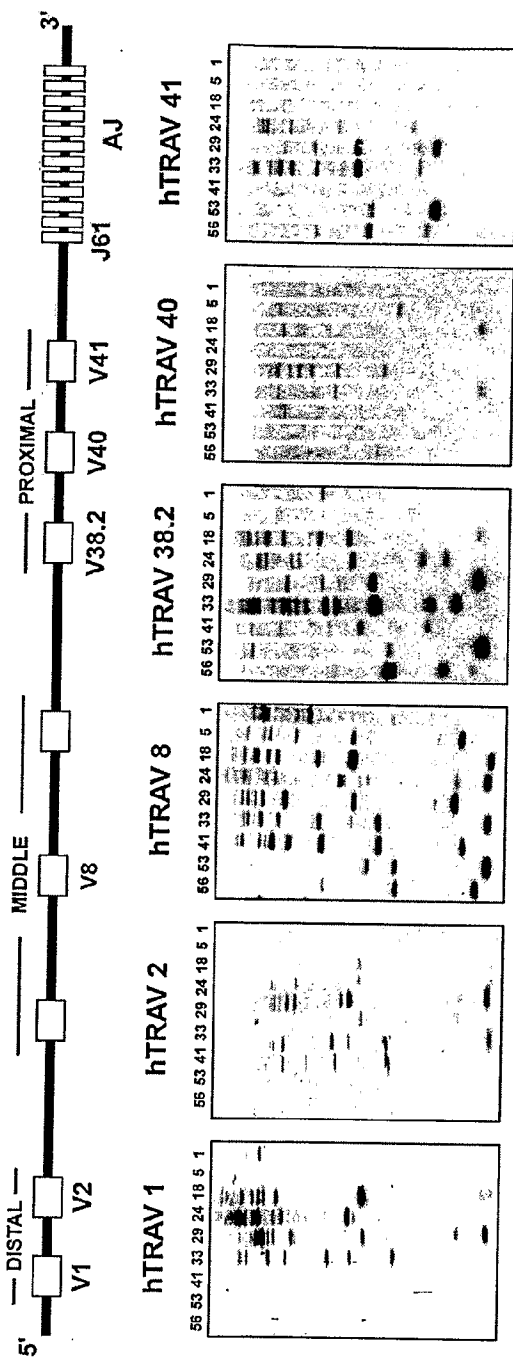


FIGURE 6

REPLACEMENT SHEET

7/8

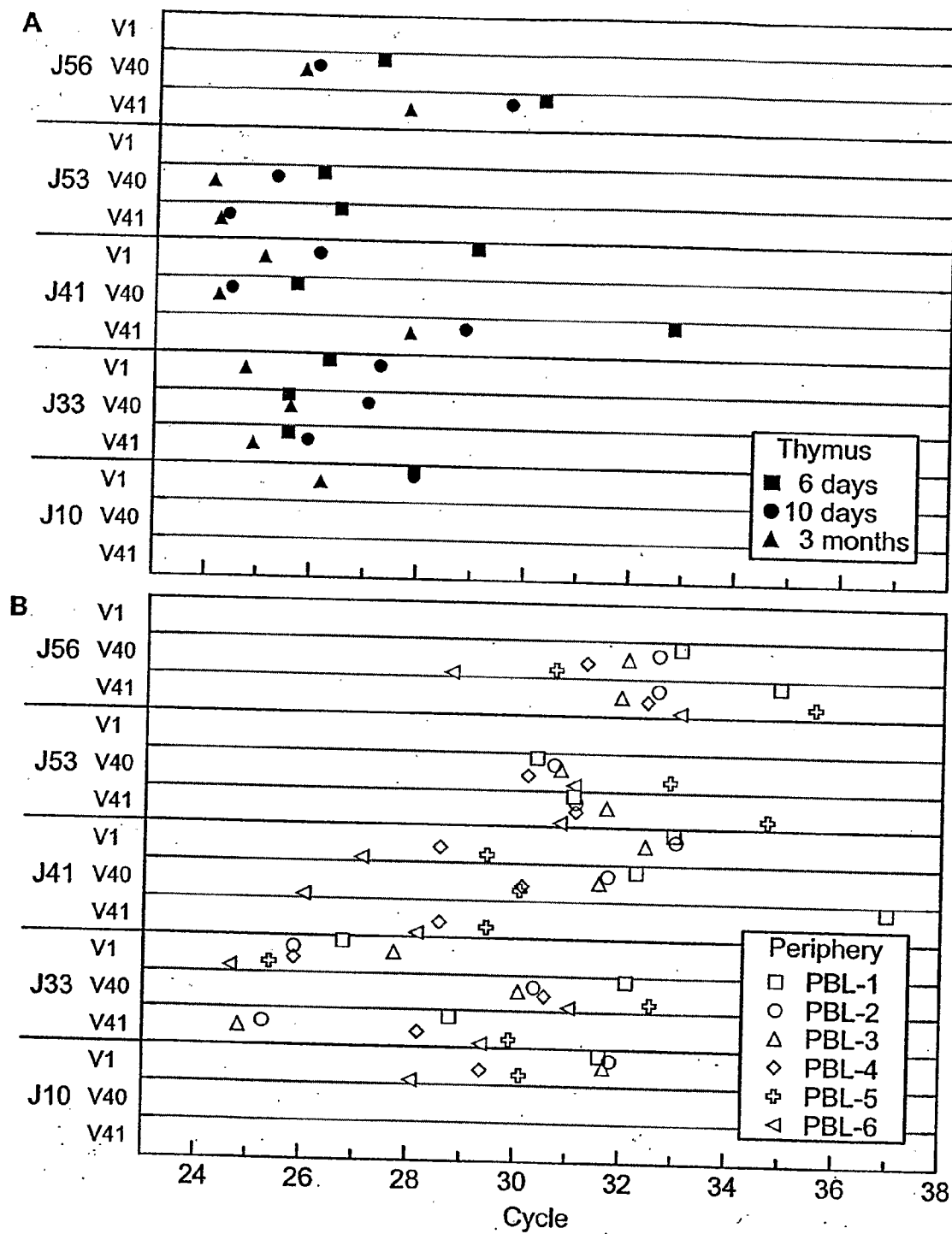


FIGURE 7

8/8

## REPLACEMENT SHEET

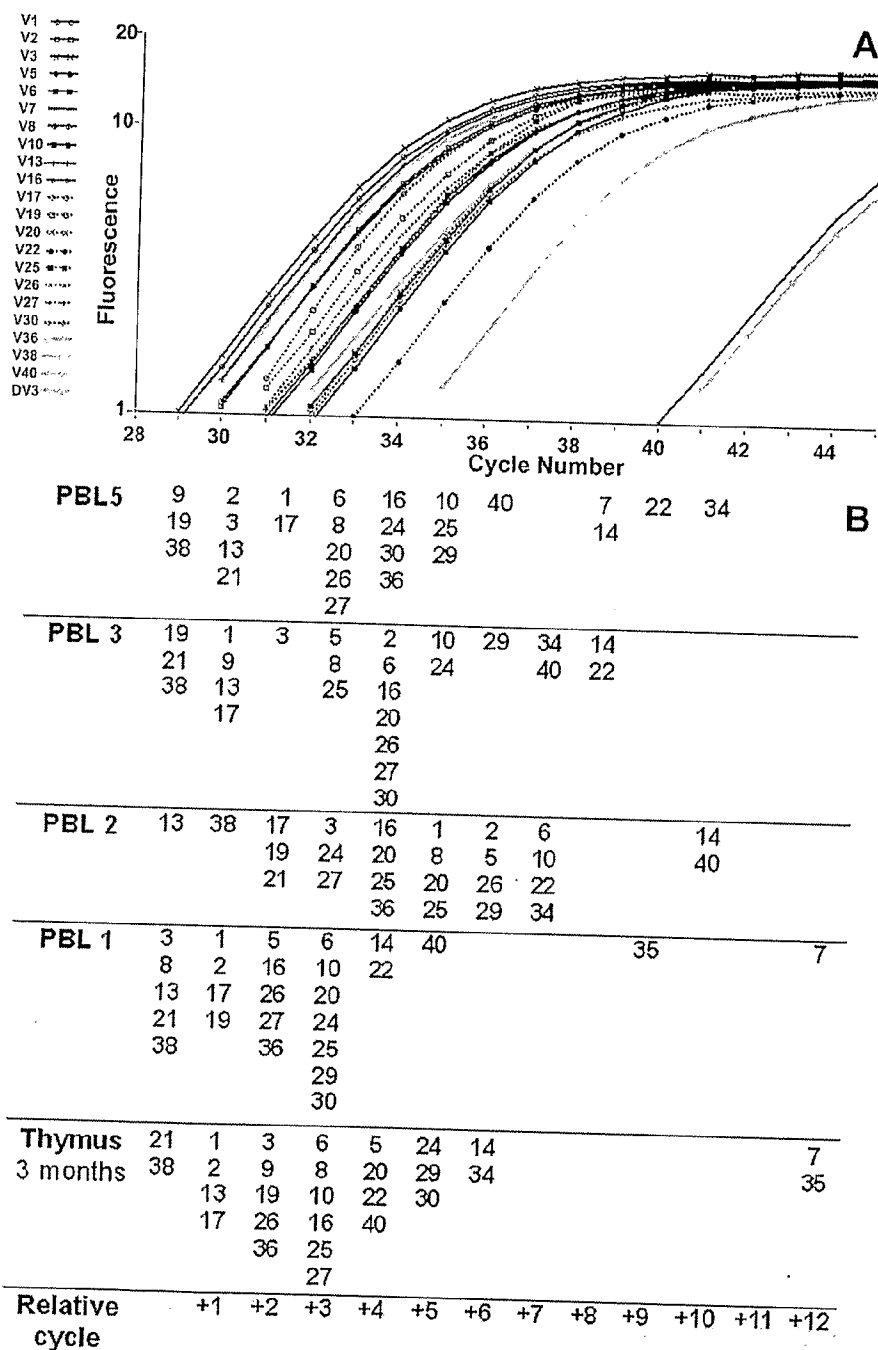


FIGURE 8